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WHAT IS CLAIMED IS:

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- 3 1. A method for detection of at least one allele of a 4 genetic locus comprising amplifying genomic DNA with an intron-spanning primer pair that defines a 5 DNA sequence, said DNA sequence being in genetic 7 linkage with said genetic locus and containing a 8 sufficient number of intron sequence nucleotides 9 to produce an amplified DNA sequence 10 characteristic of said allele.
- 11 2. The method of Claim 1 wherein said amplified DNA 12 sequence includes at least about 300 nucleotides 13 corresponding to intron sequences.
- 14 3. The method of Claim 1 wherein said intron sequence 15 is adjacent to an exon encoding said allele.
 - 4. The method of Claim 1 wherein said amplified DNA sequence is characteristic of at least one nonadjacent allele.
 - 5. The method of Claim 1 wherein said amplified DNA sequence is characteristic of at least one adjacent allele and at least one nonadjacent allele.
 - 6. The method of Claim 5 wherein said amplified DNA sequence includes at least about 1,000 nucleotides corresponding to intron sequences.
 - 7. A method for detection of at least one allele of a genetic locus comprising:
 - a. amplifying genomic DNA with an intronspanning primer pair that defines a DNA
 sequence, said DNA sequence being in genetic
 linkage with said allele and containing a
 sufficient number of intron sequence
 nucleotides to produce an amplified DNA
 sequence characteristic of said allele; and

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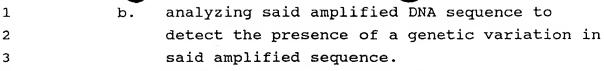
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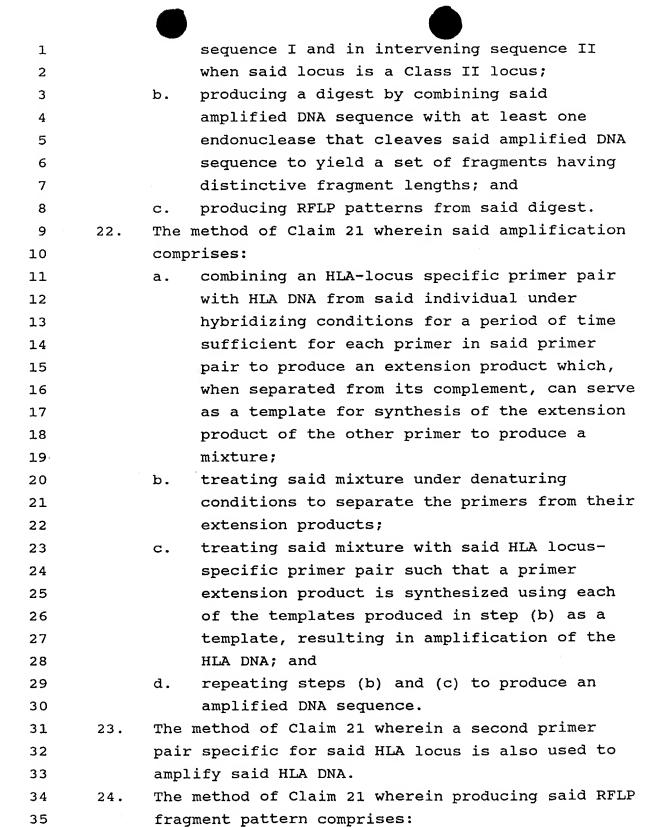
- 8. The method of Claim 7 wherein said variation in said amplified DNA sequence is a variation in the length of the primer-defined amplified DNA sequence.
- 9. The method of Claim 7 wherein said variation in said amplified DNA sequence is a change in the presence of at least one restriction site in the primer-defined amplified DNA sequence.
- 12 10. The method of Claim 7 wherein said variation in 13 said amplified DNA sequence is a change in the 14 location of at least one restriction site in the 15 primer-defined amplified DNA sequence.
 - 11. The method of Claim 7 wherein said variation in said amplified DNA sequence is a substitution of at least one nucleotide in the primer-defined amplified DNA sequence.
 - 12. The method of Claim 7 wherein said genetic locus is a major histocompatibility locus.
- The method of Claim 7 wherein said allele is associated with a monogenic disease.
- 24 14. The method of Claim 13 wherein said monogenic25 disease is cystic fibrosis.
- 26 15. The method of Claim 7 wherein at least about 70% of said primer-defined amplified DNA sequence corresponds to intron sequences.
- 29 16. The method of Claim 7 wherein said primer-defined 30 amplified DNA sequence is from 300 to 500 31 nucleotides in length.
- 32 17. A method for producing RFLP fragments for an HLA 33 locus of an individual comprising the steps of:
- a. amplifying genomic HLA DNA from said individual with a primer pair specific for

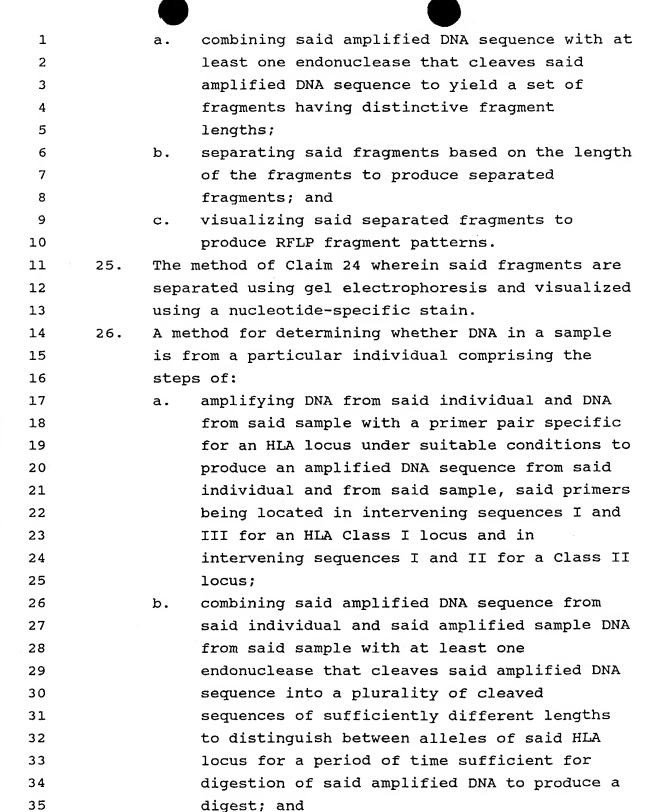
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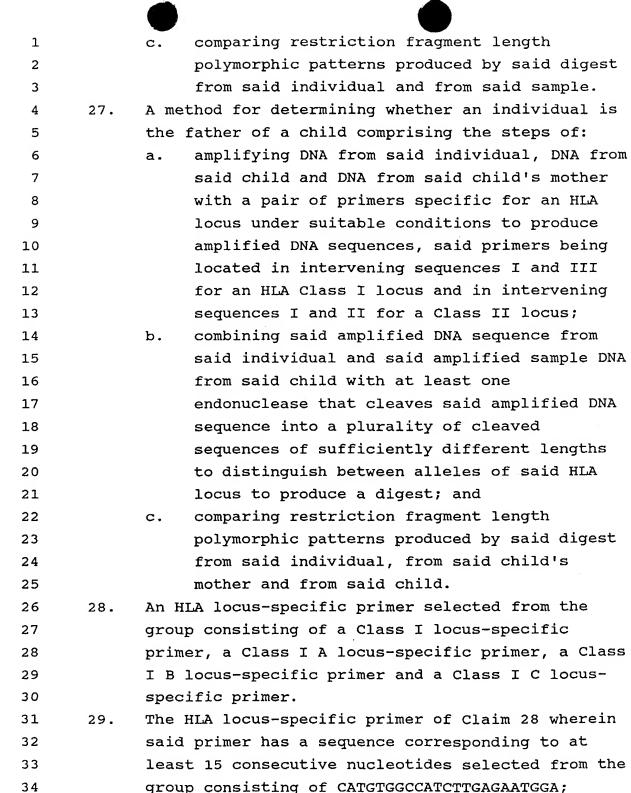
1		said HLA locus under conditions suitable to
2		produce an amplified DNA sequence; and
3		 b. producing a digest by combining said
4		amplified DNA sequence with at least one
5		endonuclease that cleaves said amplified DNA
6		sequence to yield a set of fragments having
7		distinctive fragment lengths.
8	18.	The method of Claim 17 additionally comprising the
9		step of producing RFLP patterns from said digest.
10	19.	The method of Claim 17 wherein said primers define
11		a DNA sequence that contains all exons that encode
12		allelic variability associated with said HLA
13		locus.
14	20.	A method for producing RFLP fragments for an HLA
15		locus of an individual comprising the steps of:
16		a. amplifying genomic HLA DNA from said
17		individual with a primer pair specific for
18		said HLA locus under conditions suitable to
19		produce an amplified DNA sequence, said
20		primers defining a DNA sequence that contains
21		all exons that encode allelic variability
22		associated with said HLA locus; and
23		b. producing a digest by combining said
24		amplified DNA sequence with at least one
25		endonuclease that cleaves said amplified DNA
26		sequence to yield a set of fragments having
27		distinctive fragment lengths.
28	21.	A method for producing RFLP patterns for an HLA
29		locus of an individual comprising the steps of:
30		a. amplifying HLA DNA from said individual with
31		a primer pair specific for said HLA locus
32		under conditions suitable to produce an
33		amplified DNA sequence, said primers being
34		located in intervening sequence I and in
35		intervening sequence III when said HLA locus

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is a Class I locus and in intervening







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CCAGAGAGTGACTCTGAGG; CACAATTAAGGGAT;

GCCCGGGAGATCTACAGGCGATCA; CGCCTCCCTGATCGCCTGTAG;

1		TCCCCGGCGACCTATAGGAGATGG; CTAGGACCACCCATGTGACCAGC;
2		ATCTCCTCAGACGCCGAGATGCGTCAC;
3		CTCCTGCTGCTCTGGGGGGCAG; ACTTTACCTCCACTCAGATCAGGAG;
4		CGTCCAGGCTGGTGTCTGGGTTCTGTGCCCCT;
5		CTGGTCACATGGGTGGTCCTAGG;
6		CGCCTGAATTTTCTGACTCTTCCCAT;
7		ATCCCGGGAGATCTACAGGAGATG; AACAGCGCCCATGTGACCATCCT;
8		CTGGGGAGGCGCCGCTTGAGGATTCT;
9		CGTCTCCGCAGTCCCGGTTCTAAAGTTCCCAGT;
10		ATCCTCGTGCTCTCGGGA; TGTGGTCAGGCTGCTGAC;
11		AAGGTTTGATTCCAGCTT;
12		CCCCTTCCCCACCCCAGGTGTTCCTGTCCATTCTTCAGGA;
13		CACATGGGCGCTGTTGGAGTGTCG; GTGAGTGCGGGGTCGGGAGGGA;
14		CACCCACCGGGACTCAGA; TGGCCCTGACCCAGACCTGGGC;
15		GAGGGTCGGGCGGTCTCAGC; CTCTCAGGCCTTGTTC;
16		CAGAAGTCGCTGTTCC; TTCTGAGCCAGTCCTGAGA;
17		TTGCCCTGACCACCGTGATG; CTTCCTGCTTGTCATCTTCA;
18		CCATGAATTTGATGGAGA; ACCGCTGCTACCAATGGTA;
19		CCAAGAGGTCCCCAGATC; TCATCATAGCTGTGCTGATG;
20		AGAACATGTGATCATCCAGGC; CCAACTATACTCCGATCACCAAT;
21		TGACAGTGACACTGATGGTGCTG; GGGGACACCCGACCACGTTTC;
22		TGCAGACACAACTACGGGGTTG; TGGCTGAGGGCAGAGACTCTCCC;
23		TGCTACTTCACCAACGGGAC; GGTGTGCACACACACTAC;
24		AGGTATTTTACCCAGGGACCAAGAGAT;
25		ATGTAAAATCAGCCCGACTGCCTCTTC;
26		GCCTCGTGCCTTATGCGTTTGCCTCCT;
27		TGAGGTTAATAAACTGGAGAA; GAGAGTGGCGCCTCCGCTCAT; and
28		GAGTGAGGGCTTTGGGCCGG.
29	30.	An HLA Class I locus-specific primer pair.
30	31.	An HLA Class II locus-specific, intron-spanning
31		primer pair.
32	32.	A DNA sequence defined by an HLA locus-specific
33		primer pair.
34	33.	A kit comprising at least one HLA locus-specific
35		primer pair in a suitable container, wherein said
36		HLA locus-specific primer pair is selected from

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